

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 17:05:22 ; Search time 14 Seconds  
(without alignments)  
2130.106 Million cell updates/sec

Title: US-09-831-656-2

Perfect score: 3821

Sequence: 1 MKKRLSLFVGLMLLGLF.....NHVATPTGATGNTVTWQN 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3713	97.2	717	1	AMYM_BACST
2	1737	45.5	718	1	CDGT_BACCI
3	1729	45.2	718	1	CDGT_BACSS
4	1721	45.0	710	1	CDGT_THETU
5	1688.5	44.7	718	1	CDGT_BACLI
6	1669.5	43.7	713	1	CDGT_PAEMA
7	1623	42.5	714	1	CDGI_PAEMA
8	1588.5	41.6	713	1	CDGT_BACSP
9	1585.5	41.5	713	1	CDGU_BACCI
10	1574.5	41.2	711	1	CDGT_BACST
11	1566.5	41.0	713	1	AMVR_BACS8
12	1536.5	40.2	713	1	CDGT_BACS0
13	1507	39.4	712	1	CDGT_BACS3
14	1498.5	39.2	704	1	CDGT_BACOH
15	1480.5	38.7	703	1	CDGT_BACS2
16	1160	30.4	528	1	AMY_BACCI
17	966.5	25.3	655	1	CDGT_KLEPN
18	634.5	16.6	1196	1	AMYB_PAEPO
19	480	12.6	494	1	AMVL_SACFI
20	479.5	12.5	1475	1	APU_THETU
21	477.5	12.5	919	1	AMY_STELI
22	460	12.0	1481	1	APU_THET
23	453	11.9	512	1	AMYL_DEBOC
24	451.5	11.8	1861	1	APU_THETU
25	450	11.8	499	1	AMYA_ASFOR
26	448	11.7	499	1	AMYA_ASFPH
27	444	11.6	498	1	AMYA_ASFAP
28	444	11.6	499	1	AMTB_ASFAP
29	439.5	11.5	478	1	YDDI_SCHPO
30	432	11.3	484	1	AMYA_ASFNG
31	429	11.2	1279	1	APU_THESA
32	419	11.0	581	1	AMVL_SCHPO
33	390	10.2	585	1	NEPU_THETU

34	388	10.2	569	1	AMY_STRVL
35	370.5	9.7	574	1	CDAS_THET
36	365	9.6	588	1	NEPU_BACST
37	359.5	9.4	566	1	AMY_STRLM
38	354.5	9.3	676	1	AMY1_ECOLI
39	353.5	9.3	586	1	AMY1_STRGR
40	334.5	8.8	548	1	AMT4_PSEST
41	334.5	8.8	586	1	AMYM_BACAD
42	330	8.6	562	1	AMY2_DICTH
43	326	8.5	605	1	MAL2_ECOLI
44	319.5	8.4	605	1	AMY_THETU
45	317	8.3	513	1	AMY3_SCHPO

ALIGNMENTS

RESULT 1  
AMYM\_BACST  
ID AMYM\_BACST STANDARD; PRT; 717 AA.  
AC P19531;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Maltogenic alpha-amylose precursor (EC 3.2.1.133) (Glucan 1,4-alpha-maltohydrolase).  
DE maltohydrolase).  
GN AMYM.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacillales; Geobacillus.  
OX NCBI\_TaxID=1422;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-45.  
RC STRAIN=C599;  
RA Diderichsen B., Christiansen L.;  
RT "Cloning of a maltogenic alpha-amylose from Bacillus stearothermophilus".  
RL FEMS Microbiol. Lett. 56:53-60(1988).  
CC -!- FUNCTION: CONVERTS STARCH INTO MALTOSE.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of (1->4)-alpha-D-glucosidic linkages in polysaccharides so as to remove successive alpha-maltose residues from the non-reducing ends of the chains.  
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
CC -----  
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CC -----  
CC EMBL; M36539; AAA22233.1; -;  
CC PIR; S28784; S28784.  
CC HGSP; P30920; 1CGT.  
CC InterPro; IPR000461; Alpha\_amylose.  
CC InterPro; IPR002044; CBD\_4.  
CC InterPro; IPR002909; IPT\_TIG.  
CC Pfam; PF00128; alpha-amylose; 1.  
CC Pfam; PF00686; CBM\_20; 1.  
CC Pfam; PF01833; TIG; 1.  
CC Pfam; PF02806; alpha-amylose\_C; 1.  
CC ProDom; PD001568; CBD\_4; 1.  
CC SMART; SM00429; IPT; 1.  
CC Hydroxylase; Glycosidase; Carbohydrate metabolism; Signal.  
CC SIGNAL 1 33  
CC CHAIN 34 717 MALTOGENIC ALPHA-AMYLASE.  
CC SQ SEQUENCE 717 AA; 78723 MW; 945DA8DB89BB2433 CRC64;

Query Match 97.2%; Score 3713; DB 1; Length 717;  
Best Local Similarity 98.1%; Pred. No. 2.5e-198;  
Matches 708; Conservative 2; Mismatches 4; Indels 8; Gaps 5;

QY 1 MKKTLISLVGLMLLIGLFGSLPYNPNAEASSSASVKGDVYQIIIDRFYDGDITNN 60  
 Db 1 MKKTLISLVGLMLLIGLFGSLPYNPNAEASSSASVKGDVYQIIIDRFYDGDITNN 60  
 QY 61 NPAKSYGLYDPTKSKWKMYGGDLGVRQKLPYLKQLGVTTIWLSPVLDNLDITLAGTDNT 120  
 Db 61 NPAKSYGLYDPTKSKWKMYGGDLGVRQKLPYLKQLGVTTIWLSPVLDNLDITLAGTDNT 120  
 QY 121 GYHGYWTRDPKQIEEHFGNWTFTDLVNDHQHGIKIVDFVPHNSTPFKANDSTFAEGG 180  
 Db 121 GYHGYWTRDPKQIEEHFGNWTFTDLVNDHQHGIKIVDFVPHNSTPFKANDSTFAEGG 180  
 QY 181 ALYNNCTYMGNYEDDATTGKGFHNGDISNWDDEYEAQWKNFTDPAGFSLADLSQENGTIA 240  
 Db 181 ALYNNCTYMGNYEDDATTGKGFHNGDISNWDDEYEAQWKNFTDPAGFSLADLSQENGTIA 240  
 QY 241 QYLTDAAVOLVAHAGDGLRIDAVKHFNSGFSKSLADKLYOKKIDFLVGEWYGGDPTGTAH 300  
 Db 241 QYLTDAAVOLVAHAGDGLRIDAVKHFNSGFSKSLADKLYOKKIDFLVGEWYGGDPTGTAH 300  
 QY 301 LEKVRVANNNGVNLDFDLNTVIRNVFGTFTOTMYDLNNMNVOTGNEYKYKENLITFDN 360  
 Db 298 LEKVRVANNNGVNLDFDLNTVIRNVFGTFTOTMYDLNNMNVOTGNEYKYKENLITFDN 357  
 QY 361 HDMRSFLSVNS-NKANLHQ-ALAFILTSRGT-PSIYVGTQEQYNAGNDPYNRGMMPAFDT 417  
 Db 358 HDMRSFLSVNSKANKHQLLSFSL--RGVRPPIYGTQEQYNAGNDPYNRGMMPAFDT 415  
 QY 418 TTTAPEKEVSTLAGLRNNAIIOYGTTRWINNDVYIERKFFNDVVLVAINRNTOSYS 477  
 Db 416 TTTAPEKEVSTLAGLRNNAIIOYGTTRWINNDVYIERKFFNDVVLVAINRNTOSYS 475  
 QY 478 ISGLQALPNSGYADYLSGLLGGNGISVNSGVSASFTLAPGAVSWQVYTSASAPQIGSV 537  
 Db 476 ISGLQALPNSGYADYLSGLLGGNGISVNSGVSASFTLAPGAVSWQVYTSASAPQIGSV 535  
 QY 538 APNMGIPGNVYTIIDKGFGTGTGTVFGGVTATVKSNTSRNIEVYVPPNMAAGLTDVKVTA 597  
 Db 536 APNMGIPGNVYTIIDKGFGTGTGTVFGGVTATVKSNTSRNIEVYVPPNMAAGLTDVKVTA 595  
 QY 598 GGVSSNLYSYNLSGTQSVTVTKSAPPTNLGDKIYLTGNTPELGNMSTDSGAVNNAQ 657  
 Db 596 GGVSSNLYSYNLSGTQSVTVTKSAPPTNLGDKIYLTGNTPELGNMSTDSGAVNNAQ 655  
 QY 658 GPLLAPNYPDFWYFVSYPAGTIQPFKIKRADGTIOWENSGNHVATPTGATGNITWTW 717  
 Db 656 GPLLAPNYPDFWYFVSYPAGTIQPFKIKRADGTIOWENSGNHVATPTGATGNITWTW 715  
 QY 718 QN 719  
 Db 716 QN 717

RESULT 2  
 CDGT\_BACCI STANDARD; PRT; 718 AA.  
 AC P30920;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)  
 OS (Cyclodextrin-glycosyltransferase) (CGTase).  
 OC Bacillus circulans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1397;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=8;  
 RX MEDLINE=91103970; PubMed=1368573;  
 RA Nitschke L., Heeger K., Bender H., Schulz G.E.;  
 RT "Molecular cloning, nucleotide sequence and expression in Escherichia  
 coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus  
 circulans strain no. 8."

Appl. Microbiol. Biotechnol. 33:542-546(1990).  
 [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC STRAIN=8;  
 RX MEDLINE=9111298; PubMed=1826034;  
 RA Klein C., Schulz G.E.;  
 RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A  
 resolution.";  
 RL J. Mol. Biol. 217:737-750(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).  
 RC STRAIN=8;  
 RX MEDLINE=90064533; PubMed=2531228;  
 RA Hofmann B.E., Bender H., Schulz G.E.;  
 RT "Three-dimensional structure of cyclodextrin glycosyltransferase from  
 Bacillus circulans at 3.4-A resolution.";  
 RL J. Mol. Biol. 209:793-800(1989).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RC STRAIN=8;  
 RX MEDLINE=98226626; PubMed=9558324;  
 RA Schmidt A.K., Cottaz S., Drieguez H., Schulz G.E.;  
 RT "Structure of cyclodextrin glycosyltransferase complexed with a  
 derivative of its main product beta-cyclodextrin.";  
 RL Biochemistry 37:5909-5915(1998).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RC STRAIN=8;  
 RX MEDLINE=98409292; PubMed=9738912;  
 RA Parsielegia G., Schmidt A.K., Schulz G.E.;  
 RT "Substrate binding to a cyclodextrin glycosyltransferase and  
 mutations increasing the gamma-cyclodextrin production.";  
 RL Eur. J. Biochem. 255:710-717(1998).  
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation  
 of a 1,4-alpha-D-glucosidic bond.  
 CC -1- COFACTOR: BINDS TWO CALCIUM IONS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: CETASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE  
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND  
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER  
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN  
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE  
 MALTOOLIGOSACCHARIDE PRODUCED.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC  
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 CC -----  
 CC EMBL; X68326; CAA48401.1;  
 DR PIR; S23674; ALBSCG.  
 DR PDB; 1CGT; 31-JAN-94.  
 DR PDB; 1CGU; 31-JAN-94.  
 DR PDB; 3CGT; 27-MAY-98.  
 DR PDB; 4CGT; 12-AUG-98.  
 DR PDB; 5CGT; 12-AUG-98.  
 DR PDB; 6CGT; 14-OCT-98.  
 DR PDB; 7CGT; 12-AUG-98.  
 DR PDB; 8CGT; 14-OCT-98.  
 DR PDB; 9CGT; 14-OCT-98.  
 DR InterPro; IPR000461; Alpha\_amylase.  
 DR InterPro; IPR002044; CBD\_4.  
 DR InterPro; IPR002909; IPT\_TIG.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF00686; CBM\_20; 1.  
 DR Pfam; PF01833; TIG; 1.  
 DR Pfam; PF02806; alpha-amylase\_C; 1.  
 DR ProDom; PD001568; CBD\_4; 1.